SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Goli, Surya K.
Hillman, Jennifer L.
Murry, Lynn E.

(ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID RECEPTOR PROTEIN

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0233 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: CONUTUT01
(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
 1               5                  10                  15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
            20                  25                  30
```

```
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
          35                  40                  45
Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro
      50                  55                  60
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
65                  70                  75                  80
Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
                85                  90                  95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
            100                 105                 110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
        115                 120                 125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
    130                 135                 140
Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
145                 150                 155                 160
Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
                165                 170                 175
Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg
            180                 185                 190
Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala
        195                 200                 205
Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: CONUTUT01
(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GCCGCCGAAC CCCGCGCGCC ACTCGCTCGC TCAGAGGGAG GAGAAAGTGG CGAGTTCCGG     60
ATCCCTGCCT AGCGCGGCCC AACCTTTACT CCAGAGATCA TGGCTGCCGA GGATGTGGTG    120
GCGACTGGCG CCGACCCAAG CGATCTGGAG AGCGGCGGGC TGCTGCATGA GATTTTCACG    180
TCGCCGCTCA ACCTGCTGCT GCTTGGCCTC TGCATCTTCC TGCTCTACAA GATCGTGCGC    240
GGGGACCAGC CGGCGGCCAG CGGCGACAGG ACGACGACGA NGCCGCCCCC TCTGCCCCGC    300
CTCAAGCGGC GCGACTTCAC CCCCGCCGAG CTGCGGCGCT TCGACGGCGT CCAGGACCCG    360
CGCATACTCA TGGCCATCAA CGGCAAGGTG TTCGATGTGA CCAAAGGCCG CAAATTCTAC    420
GGGCCCGAGG GGCCGTATGG GGTCTTTGCT GGAAGAGATG CATCCAGGGG CCTTGCCACA    480
TTTTGCCTGG ATAAGGAAGC ACTGAAGGAT GAGTACGATG ACCTTTCTGA CCTCACTGCT    540
GCCCAGCAGG AGACTCTGAG TGACTGGGAG TCTCAGTTCA CTTTCAAGTA TCATCACGTG    600
GGCAAACTGC TGAAGGAGGG GGAGGAGCCC ACTGTGTACT CAGATGAGGA AGAACCAAAA    660
GATGAGAGTT CCCGGAAAAA TGTTAAAGCA TTCAGTGGAA GTATATCTAT NNTGTATTTT    720
GCAAAATCAT TTGTAACAGT CCACTNTGTC TTTAAAACAT AGTGTTACAA TATTTAGAAA    780
GTTTGAGC                                                             788
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 1518818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Glu Leu
 1               5                  10                  15
Glu Gly Gly Gly Leu Leu Gln Glu Ile Phe Thr Ser Pro Leu Asn Leu
            20                  25                  30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
        35                  40                  45
Asp Gln Pro Gly Ala Ser Gly Asp Asn Asp Asp Asp Glu Pro Pro Pro
    50                  55                  60
Leu Pro Arg Leu Lys Pro Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
65                  70                  75                  80
Tyr Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
                85                  90                  95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
            100                 105                 110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
        115                 120                 125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
    130                 135                 140
Leu Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe
145                 150                 155                 160
Ser Ser Pro Ser Ser Thr Ile Thr Trp Gly Lys Leu Leu Glu Gly Ala
                165                 170                 175
Glu Glu Pro Ile Val Tyr Ser Asp Asp Glu Glu Gln Lys Met Arg Leu
            180                 185                 190
Leu Gly Arg Val Thr Glu Ala Val Ser Gly Ala Tyr Leu Phe Leu Tyr
        195                 200                 205
Phe Ala Lys Ser Phe Val Thr Phe Gln Ser Val Phe Thr Thr Trp
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 1657409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ala Ala Glu Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu
 1               5                  10                  15
Glu Gly Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
            20                  25                  30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
        35                  40                  45
Asp Gln Pro Ala Ala Ser Asp Ser Asp Asp Asp Glu Pro Pro Pro Leu
    50                  55                  60
Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe
65                  70                  75                  80
Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val
                85                  90                  95
Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr
            100                 105                 110
Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys
        115                 120                 125
Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu
    130                 135                 140
Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr
145                 150                 155                 160
Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro
                165                 170                 175
Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys
            180                 185                 190
```

Asn Asp